# Phyre$^2$

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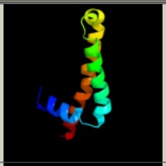
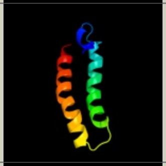
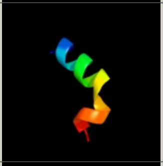
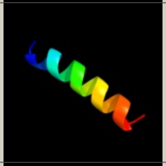
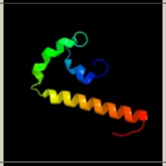
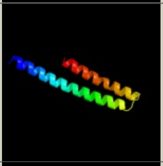
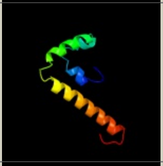
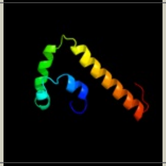
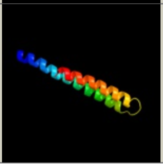
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0ACW6 |
| Date | Thu Jan 5 11:19:17 GMT 2012 |
| Unique Job ID | 1dc402a5b0f4f22e |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1zhcA_ | Alignment |  | 100.0 | 47 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein hp1242;<br>**PDBTitle:** solution structure of hp1242 from helicobacter pylori |
| 2 | c2a3dA_ | Alignment |  | 59.9 | 14 | **PDB header:**three-helix bundle<br>**Chain:** A: **PDB Molecule:**protein (de novo three-helix bundle);<br>**PDBTitle:** solution structure of a de novo designed single chain three-2 helix bundle (a3d) |
| 3 | c1yybA_ | Alignment |  | 42.1 | 20 | **PDB header:**apoptosis<br>**Chain:** A: **PDB Molecule:**programmed cell death protein 5;<br>**PDBTitle:** solution structure of 1-26 fragment of human programmed2 cell death 5 protein |
| 4 | c3ddsB_ | Alignment |  | 42.0 | 14 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**glycogen phosphorylase, liver form;<br>**PDBTitle:** crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261 |
| 5 | c3dd7D_ | Alignment |  | 41.7 | 33 | **PDB header:**ribosome inhibitor<br>**Chain:** D: **PDB Molecule:**prevent host death protein;<br>**PDBTitle:** structure of doch66y in complex with the c-terminal domain of phd |
| 6 | c2xusA_ | Alignment |  | 38.9 | 26 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**breast cancer metastasis-suppressor 1;<br>**PDBTitle:** crystal structure of the brms1 n-terminal region |
| 7 | c2c4mA_ | Alignment |  | 35.9 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**glycogen phosphorylase;<br>**PDBTitle:** starch phosphorylase: structural studies explain oxyanion-2 dependent kinetic stability and regulatory control. |
| 8 | d1hx1b_ | Alignment |  | 35.8 | 14 | **Fold:**Spectrin repeat-like<br>**Superfamily:**BAG domain<br>**Family:**BAG domain |
| 9 | d2atia1 | Alignment |  | 34.0 | 14 | **Fold:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Family:**Oligosaccharide phosphorylase |
| 10 | d2gj4a1 | Alignment |  | 30.2 | 13 | **Fold:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Family:**Oligosaccharide phosphorylase |
| 11 | d1i6za_ | Alignment |  | 22.3 | 14 | **Fold:**Spectrin repeat-like<br>**Superfamily:**BAG domain<br>**Family:**BAG domain |

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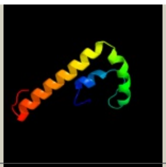
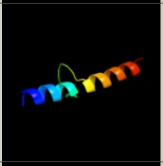
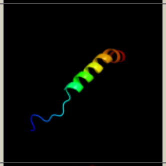
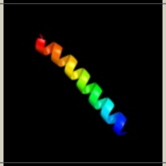
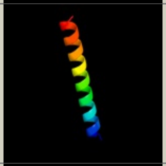
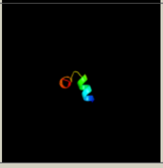
| 12 | d1l5wa_ | Alignment |  | 20.0 | 16 | **Fold:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Family:**Oligosaccharide phosphorylase |
| 13 | c3he5A_ | Alignment |  | 19.4 | 39 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**synzip1;<br>**PDBTitle:** heterospecific coiled-coil pair synzip2:synzip1 |
| 14 | c3swfA_ | Alignment |  | 17.2 | 19 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**cgmp-gated cation channel alpha-1;<br>**PDBTitle:** cnga1 621-690 containing clz domain |
| 15 | c3bbpF_ | Alignment |  | 14.6 | 25 | **PDB header:**protein transport/splicing<br>**Chain:** F: **PDB Molecule:**grip and coiled-coil domain-containing protein 2;<br>**PDBTitle:** rab6-gtp:gcc185 rab binding domain complex |
| 16 | c3pxpA_ | Alignment |  | 14.2 | 13 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**helix-turn-helix domain protein;<br>**PDBTitle:** crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution |
| 17 | c3swyB_ | Alignment |  | 13.0 | 23 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**cyclic nucleotide-gated cation channel alpha-3;<br>**PDBTitle:** cnga3 626-672 containing clz domain |
| 18 | c3dd7B_ | Alignment |  | 12.7 | 35 | **PDB header:**ribosome inhibitor<br>**Chain:** B: **PDB Molecule:**prevent host death protein;<br>**PDBTitle:** structure of doch66y in complex with the c-terminal domain of phd |
| 19 | c3nmdA_ | Alignment |  | 10.0 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**cgmp dependent protein kinase;<br>**PDBTitle:** crystal structure of the leucine zipper domain of cgmp dependent2 protein kinase i beta |
| 20 | d1xbra_ | Alignment |  | 9.2 | 26 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**p53-like transcription factors<br>**Family:**T-box |
| 21 | c2w6aB_ | Alignment | not modelled | 9.1 | 26 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**arf gtpase-activating protein git1;<br>**PDBTitle:** x-ray structure of the dimeric git1 coiled-coil domain |
| 22 | d1or7a2 | Alignment | not modelled | 8.1 | 17 | **Fold:**Sigma2 domain of RNA polymerase sigma factors<br>**Superfamily:**Sigma2 domain of RNA polymerase sigma factors<br>**Family:**Sigma2 domain of RNA polymerase sigma factors |
| 23 | c2kq6A_ | Alignment | not modelled | 6.7 | 19 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**polycystin-2;<br>**PDBTitle:** the structure of the ef-hand domain of polycystin-2 suggests a2 mechanism for ca2+-dependent regulation of polycystin-2 channel3 activity |
| 24 | c3d7iB_ | Alignment | not modelled | 5.8 | 13 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**carboxymuconolactone decarboxylase family protein;<br>**PDBTitle:** crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution |
| 25 | c1ny9A_ | Alignment | not modelled | 5.7 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional activator tipa-s;<br>**PDBTitle:** antibiotic binding domain of a tipa-class multidrug2 resistance transcriptional regulator |
| 26 | d1ny9a_ | Alignment | not modelled | 5.7 | 17 | **Fold:**Antibiotic binding domain of TipA-like multidrug resistance regulators<br>**Superfamily:**Antibiotic binding domain of TipA-like multidrug resistance regulators<br>**Family:**Antibiotic binding domain of TipA-like multidrug resistance regulators |
| 27 | c2f9jP_ | Alignment | not modelled | 5.5 | 11 | **PDB header:**rna binding protein<br>**Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1;<br>**PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of |

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| | | | | | | the spliceosomal2 protein p14 bound to a region of sf3b155 |
| 28 | d1or7b2 | Alignment | not modelled | 5.3 | 15 | **Fold:**Sigma2 domain of RNA polymerase sigma factors<br>**Superfamily:**Sigma2 domain of RNA polymerase sigma factors<br>**Family:**Sigma2 domain of RNA polymerase sigma factors |
| 29 | d1h6fa_ | Alignment | not modelled | 5.2 | 41 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**p53-like transcription factors<br>**Family:**T-box |